Schwartzman

#7

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/192,611*

DATE: 03/01/2000 3/2/00
TIME: 12:43:34

INPUT SET: S34907.raw

> **This Raw Listing contains the General
> Information Section and up to the first 5 pages.**

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 1                          SEQUENCE LISTING
 2
 3    (1)    General Information:                ENTERED
 4
 5       (i) APPLICANT:        Glimcher, Laurie H.
 6                             Hodge, Martin R.
 7
 8      (ii) TITLE OF INVENTION:  NF-AT-INTERACTING PROTEIN NIP45 AND METHODS
 9                                OF USE THEREFOR
10
11     (iii) NUMBER OF SEQUENCES: 2
12
13      (iv) CORRESPONDENCE ADDRESS:
14              (A) ADDRESSEE: LAHIVE & COCKFIELD
15              (B) STREET: 60 State Street, suite 510
16              (C) CITY: Boston
17              (D) STATE: Massachusetts
18              (E) COUNTRY: USA
19              (F) ZIP: 02109-1875
20
21       (v) COMPUTER READABLE FORM:
22              (A) MEDIUM TYPE: Floppy disk
23              (B) COMPUTER: IBM PC compatible
24              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25              (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
26
27      (vi) CURRENT APPLICATION DATA:
28              (A) APPLICATION NUMBER: 09/192,611
29              (B) FILING DATE:
30              (C) CLASSIFICATION:
31
32     (vii) PRIOR APPLICATION DATA:
33              (A) APPLICATION NUMBER: US/08/755,584
34              (B) FILING DATE:
35
36    (viii) ATTORNEY/AGENT INFORMATION:
37              (A) NAME: Giulio A. DeConti, Jr.
38              (B) REGISTRATION NUMBER: 31,503
39              (C) REFERENCE/DOCKET NUMBER: HUI-026
40
41      (ix) TELECOMMUNICATION INFORMATION:
42              (A) TELEPHONE: (617)227-7400
43              (B) TELEFAX: (617)227-5941
44
45
46    (2) INFORMATION FOR SEQ ID NO:1:
```

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/09/192,611*

INPUT SET: S34907.raw

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47
48          (i) SEQUENCE CHARACTERISTICS:
49              (A) LENGTH: 1946 base pairs
50              (B) TYPE: nucleic acid
51              (C) STRANDEDNESS: single
52              (D) TOPOLOGY: linear
53
54         (ii) MOLECULE TYPE: cDNA
55
56         (ix) FEATURE:
57              (A) NAME/KEY: CDS
58              (B) LOCATION: 13..1248
59
60
61         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62
63   ACAGTGTGGG AG ATG GCG GAA CCA CTG AGG GGA CGT GGT CCG AGG TCC          48
64                 Met Ala Glu Pro Leu Arg Gly Arg Gly Pro Arg Ser
65                  1               5                  10
66
67   CGC GGT GGC CGA GGC GCT CGG AGA GCC CGA GGC GCC CGT GGC CGG TGT        96
68   Arg Gly Gly Arg Gly Ala Arg Arg Ala Arg Gly Ala Arg Gly Arg Cys
69           15              20                  25
70
71   CCT CGC GCC CGG CAG TCT CCG GCT AGG CTC ATT CCA GAC ACC GTG CTT       144
72   Pro Arg Ala Arg Gln Ser Pro Ala Arg Leu Ile Pro Asp Thr Val Leu
73       30                  35                  40
74
75   GTG GAC TTG GTC AGT GAC AGC GAC GAA GAG GTC TTG GAA GTC GCA GAC       192
76   Val Asp Leu Val Ser Asp Ser Asp Glu Glu Val Leu Glu Val Ala Asp
77    45                  50                  55                  60
78
79   CCA GTA GAG GTG CCG GTC GCC CGC CTC CCC GCG CCG GCT AAA CCT GAG       240
80   Pro Val Glu Val Pro Val Ala Arg Leu Pro Ala Pro Ala Lys Pro Glu
81                   65                  70                  75
82
83   CAG GAC AGC GAC AGT GAC AGT GAA GGG GCG GCC GAG GGG CCT GCG GGA       288
84   Gln Asp Ser Asp Ser Asp Ser Glu Gly Ala Ala Glu Gly Pro Ala Gly
85                   80                  85                  90
86
87   GCC CCG CGT ACA TTG GTG CGA CGG CGG CGG CGG CGG CTG CTG GAT CCC       336
88   Ala Pro Arg Thr Leu Val Arg Arg Arg Arg Arg Arg Leu Leu Asp Pro
89           95                  100                 105
90
91   GGA GAG GCG CCG GTG GTC CCA GTG TAC TCC GGG AAG GTA CAG AGC AGC       384
92   Gly Glu Ala Pro Val Val Pro Val Tyr Ser Gly Lys Val Gln Ser Ser
93       110                 115                 120
94
95   CTC AAC CTC ATT CCA GAT AAT TCA TCC CTC TTG AAA CTG TGC CCT TCA       432
96   Leu Asn Leu Ile Pro Asp Asn Ser Ser Leu Leu Lys Leu Cys Pro Ser
97   125                 130                 135                 140
98
99   GAG CCT GAA GAT GAG GCA GAT CTG ACA AAT TCT GGC AGT TCT CCC TCT       480
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INPUT SET: S34907.raw

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100   Glu Pro Glu Asp Glu Ala Asp Leu Thr Asn Ser Gly Ser Ser Pro Ser
101               145             150                 155
102
103   GAG GAT GAT GCC CTG CCT TCA GGT TCT CCC TGG AGA AAG AAG CTC AGA        528
104   Glu Asp Asp Ala Leu Pro Ser Gly Ser Pro Trp Arg Lys Lys Leu Arg
105               160             165                 170
106
107   AAG AAG TGT GAG AAA GAA GAA AAG AAA ATG GAA GAG TTT CCG GAC CAG        576
108   Lys Lys Cys Glu Lys Glu Glu Lys Lys Met Glu Glu Phe Pro Asp Gln
109           175             180                 185
110
111   GAC ATC TCT CCT TTG CCC CAA CCT TCG TCA AGG AAC AAA AGC AGA AAG        624
112   Asp Ile Ser Pro Leu Pro Gln Pro Ser Ser Arg Asn Lys Ser Arg Lys
113       190             195                 200
114
115   CAT ACG GAG GCG CTC CAG AAG CTA AGG GAA GTG AAC AAG CGT CTC CAA        672
116   His Thr Glu Ala Leu Gln Lys Leu Arg Glu Val Asn Lys Arg Leu Gln
117   205             210                 215                 220
118
119   GAT CTC CGC TCC TGC CTG AGC CCC AAG CAG CAC CAG AGT CCA GCC CTT        720
120   Asp Leu Arg Ser Cys Leu Ser Pro Lys Gln His Gln Ser Pro Ala Leu
121               225             230                 235
122
123   CAG AGC ACA GAT GAT GAG GTG GTC CTA GTG GAA GGG CCT GTC TTG CCA        768
124   Gln Ser Thr Asp Asp Glu Val Val Leu Val Glu Gly Pro Val Leu Pro
125               240             245                 250
126
127   CAG AGC TCT CGA CTC TTT ACA CTC AAG ATC CGG TGC CGG GCT GAC CTA        816
128   Gln Ser Ser Arg Leu Phe Thr Leu Lys Ile Arg Cys Arg Ala Asp Leu
129           255             260                 265
130
131   GTG AGA CTG CCT GTC AGG ATG TCG GAG CCC CTT CAG AAT GTG GTG GAT        864
132   Val Arg Leu Pro Val Arg Met Ser Glu Pro Leu Gln Asn Val Val Asp
133       270             275                 280
134
135   CAC ATG GCC AAT CAT CTT GGG GTG TCT CCA AAC AGG ATT CTT TTG CTT        912
136   His Met Ala Asn His Leu Gly Val Ser Pro Asn Arg Ile Leu Leu Leu
137   285             290                 295                 300
138
139   TTT GGA GAG AGT GAA CTG TCT CCT ACT GCC ACC CCT AGT ACC CTA AAG        960
140   Phe Gly Glu Ser Glu Leu Ser Pro Thr Ala Thr Pro Ser Thr Leu Lys
141               305             310                 315
142
143   CTT GGA GTG GCT GAC ATC ATT GAT TGT GTG GTG CTA GCA AGC TCT TCA        1008
144   Leu Gly Val Ala Asp Ile Ile Asp Cys Val Val Leu Ala Ser Ser Ser
145               320             325                 330
146
147   GAG GCC ACA GAG ACA TCC CAG GAG CTC CGG CTC CGG GTG CAG GGG AAG        1056
148   Glu Ala Thr Glu Thr Ser Gln Glu Leu Arg Leu Arg Val Gln Gly Lys
149           335             340                 345
150
151   GAG AAA CAC CAG ATG TTG GAG ATC TCA CTG TCT CCT GAT TCT CCT CTT        1104
152   Glu Lys His Gln Met Leu Glu Ile Ser Leu Ser Pro Asp Ser Pro Leu
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INPUT SET: S34907.raw

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153          350                    355                    360
154
155   AAG GTT CTC ATG TCA CAC TAT GAG GAA GCC ATG GGA CTC TCT GGA CAC   1152
156   Lys Val Leu Met Ser His Tyr Glu Glu Ala Met Gly Leu Ser Gly His
157   365                  370                  375                  380
158
159   AAG CTC TCC TTC TTC TTT GAT GGG ACA AAG CTT TCA GGC AAG GAG CTG   1200
160   Lys Leu Ser Phe Phe Phe Asp Gly Thr Lys Leu Ser Gly Lys Glu Leu
161                  385                  390                  395
162
163   CCA GCT GAT CTG GGC CTG GAA TCC GGA GAT CTC ATC GAA GTC TGG GGC   1248
164   Pro Ala Asp Leu Gly Leu Glu Ser Gly Asp Leu Ile Glu Val Trp Gly
165                  400                  405                  410
166
167   TGAAGCTCTC ACCCTGTTCG GACGCAAAGC CAAGACATGG AGACAATAGC TCCCAATTTT   1308
168
169   ATTATTGTGA TTTTTCGCCC CATAAGGGCT AACAGAAACT GAATTAGAAC TTGTTTACTT   1368
170
171   ATTTATTTCT GGTGCTGGGG ATTGAACCCC AGACTATGCA CATGCTAAGG ATGTATGAAG   1428
172
173   TGGAGGCAAA ACCAAGGCAT TACCTTTAGC CAGCCTCTAG TAGACTGTAG TGTCAAGCAA   1488
174
175   GTGGCTACTT GGTAGTTGTG TGGCTCTGTG TATGTTTGTG CTGTATTTGG CAGCCCCTGG   1548
176
177   GGCACATAGA AGGGACCTTG GCTTCCCTAC CATTTCACGT TCGCTGGTGC CCTTTCCTTC   1608
178
179   ATCAGATGAC TTCTGTGAAG CTGCCTATGT TGAGTGTGTT GAACTAAATG AGCTCTGCTT   1668
180
181   TGGGTGTCCA GGCCTGGGGT TTGTGCCGCA GTTGGAGCCA GCAGTGACTT CACTCTGACT   1728
182
183   TGGGACTGAG AATGCATTTC CTGGTGGAGA CACTCGGGTG CAGAAATATA ACAGAAGGTG   1788
184
185   ACATACATGC TGAAGCTGAG GACTAGGTCG AAAGTTAACG ACGTTGCATT TTCAGCCTTG   1848
186
187   GGTATCCTCT CTGCCTGCCA GGACTCTAGC CAGTGTCTGG TACACACTTC TTGGCATGGA   1908
188
189   CACCTAGGTC GACGCGGGCG CGATTCGGCC GACTCGAG                          1946
190
191
192   (2) INFORMATION FOR SEQ ID NO:2:
193
194        (i) SEQUENCE CHARACTERISTICS:
195            (A) LENGTH: 412 amino acids
196            (B) TYPE: amino acid
197            (D) TOPOLOGY: linear
198
199        (ii) MOLECULE TYPE: protein
200
201        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
202
203   Met Ala Glu Pro Leu Arg Gly Arg Gly Pro Arg Ser Arg Gly Gly Arg
204    1               5                  10                  15
205
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INPUT SET: S34907.raw

```
206   Gly Ala Arg Arg Ala Arg Gly Ala Arg Gly Arg Cys Pro Arg Ala Arg
207           20          25          30
208
209   Gln Ser Pro Ala Arg Leu Ile Pro Asp Thr Val Leu Val Asp Leu Val
210           35          40          45
211
212   Ser Asp Ser Asp Glu Glu Val Leu Glu Val Ala Asp Pro Val Glu Val
213           50          55          60
214
215   Pro Val Ala Arg Leu Pro Ala Pro Ala Lys Pro Glu Gln Asp Ser Asp
216    65          70          75          80
217
218   Ser Asp Ser Glu Gly Ala Ala Glu Gly Pro Ala Gly Ala Pro Arg Thr
219           85          90          95
220
221   Leu Val Arg Arg Arg Arg Arg Arg Leu Leu Asp Pro Gly Glu Ala Pro
222           100         105         110
223
224   Val Val Pro Val Tyr Ser Gly Lys Val Gln Ser Ser Leu Asn Leu Ile
225           115         120         125
226
227   Pro Asp Asn Ser Ser Leu Leu Lys Leu Cys Pro Ser Glu Pro Glu Asp
228       130         135         140
229
230   Glu Ala Asp Leu Thr Asn Ser Gly Ser Ser Pro Ser Glu Asp Asp Ala
231   145         150         155         160
232
233   Leu Pro Ser Gly Ser Pro Trp Arg Lys Lys Leu Arg Lys Lys Cys Glu
234           165         170         175
235
236   Lys Glu Glu Lys Lys Met Glu Glu Phe Pro Asp Gln Asp Ile Ser Pro
237           180         185         190
238
239   Leu Pro Gln Pro Ser Ser Arg Asn Lys Ser Arg Lys His Thr Glu Ala
240           195         200         205
241
242   Leu Gln Lys Leu Arg Glu Val Asn Lys Arg Leu Gln Asp Leu Arg Ser
243       210         215         220
244
245   Cys Leu Ser Pro Lys Gln His Gln Ser Pro Ala Leu Gln Ser Thr Asp
246   225         230         235         240
247
248   Asp Glu Val Val Leu Val Glu Gly Pro Val Leu Pro Gln Ser Ser Arg
249           245         250         255
250
251   Leu Phe Thr Leu Lys Ile Arg Cys Arg Ala Asp Leu Val Arg Leu Pro
252           260         265         270
253
254   Val Arg Met Ser Glu Pro Leu Gln Asn Val Val Asp His Met Ala Asn
255       275         280         285
256
257   His Leu Gly Val Ser Pro Asn Arg Ile Leu Leu Leu Phe Gly Glu Ser
258       290         295         300
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/192,611*

INPUT SET: S34907.raw

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